



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/804,762

DATE: 07/27/2004

TIME: 12:46:57

Input Set : A:\A-72186.ST25.txt

Output Set: N:\CRF4\07272004\J804762.raw

3 <110> APPLICANT: Qi, Yan
 4 Zhang, Xianghua
 5 Konigsberg, Paula
 7 <120> TITLE OF INVENTION: Specific Inhibition of Allorejection
 9 <130> FILE REFERENCE: A-72186/TAL/DCF (471702-00005)
 11 <140> CURRENT APPLICATION NUMBER: US 10/804,762
 12 <141> CURRENT FILING DATE: 2004-03-19
 14 <150> PRIOR APPLICATION NUMBER: US 60/456,378
 15 <151> PRIOR FILING DATE: 2003-03-19
 17 <160> NUMBER OF SEQ ID NOS: 32
 19 <170> SOFTWARE: PatentIn version 3.2
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 235
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Homo sapiens
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 33 20 25 30
 36 Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
 37 35 40 45
 40 Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
 41 50 55 60
 44 Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
 45 65 70 75 80
 48 Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
 49 85 90 95
 52 Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
 53 100 105 110
 56 Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
 57 115 120 125
 60 Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
 61 130 135 140
 64 Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
 65 145 150 155 160
 68 Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
 69 165 170 175
 72 Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
 73 180 185 190
 76 Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His
 77 195 200 205
 80 Arg Asn Arg Arg Arg Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser

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98 tggccttacc agtgaccgcc ttgctcctgc cgctggcctt gctgctccac gccgccaggc      180
100 cgagccagtt ccgggtgtcg ccgctggatc ggacctggaa cctgggcgag acagtggagc      240
102 tgaagtgccg ggtgctgctg tccaaccgca cgtcgggctg ctgctggctc tccagccgc      300
104 gcggcgccgc cgccagtcct accttctctc tatacctctc ccaaaacaag cccaaggcgg      360
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114 cagaggcgct ccggccagcg gcggggggcg cagtgcacac gagggggctg gacttcgcct      660
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154 caactagcag atacaggat gaggcagacc tgactctctt aaggaggctg agagcccaaa      1860
156 ctgctgtccc aaacatgcac ttccttgctt aagggtatgtt acaagcaatg cctgcccatt      1920
158 ggagagaaaa aacttaagta gataaggaaa taagaaccac tcataattct tcaccttagg      1980
160 aataatctcc tgttaatatg gtgtacattc ttctgatta ttttctacac atacatgtaa      2040
162 aatatgtctt tcttttttaa atagggttgt actatgctgt tatgagtggc tttaatgaat      2100
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171 <210> SEQ ID NO: 3
172 <211> LENGTH: 198
173 <212> TYPE: PRT

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Input Set : A:\A-72186.ST25.txt

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183 20 25 30
186 Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
187 35 40 45
190 Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
191 50 55 60
194 Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
195 65 70 75 80
198 Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
199 85 90 95
202 Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
203 100 105 110
206 Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
207 115 120 125
210 Val Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg
211 130 135 140
214 Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
215 145 150 155 160
218 Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Gly Asn Arg Arg Arg
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222 Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser Gly Asp Lys Pro Ser
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226 Leu Ser Ala Arg Tyr Val
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235 <400> SEQUENCE: 4
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240 tggcettacc agtgaccgcc ttgctcctgc cgctggcctt gctgctccac gccgccaggc 180
242 cgagccagtt ccgggtgtcg ccgctggatc ggacctggaa cctgggcgag acagtggagc 240
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256 cagaggcgtg ccggccagcg gcggggggcg cagggaaccg aagacgtgtt tgcaaatgtc 660
258 cccggcctgt ggtcaaactg ggagacaagc ccagcctttc ggcgagatac gtctaaccct 720
260 gtgcaacagc cactacatta cttcaaactg agatccttcc ttttgaggga gcaagtctt 780
262 ccctttcatt ttttccagtc ttctccctg tgtattcatt ctcatgatta ttattttagt 840
264 gggggcgggg tgggaaagat tactttttct ttatgtgttt gacgggaaac aaaactaggt 900
266 aaaatctaca gtacaccaca agggtcacaa tactgttgtg cgcacatcgc ggtagggcgt 960

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268 ggaaaggggc aggccagagc taccgcgaga gttctcagaa tcatgctgag agagctggag 1020
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276 gtctcagggt gaggtgcttg agtctccaac ggcaaggga caagtacttc ttgatacctg 1260
278 ggatactgtg cccagagcct cgaggaggta atgaattaaa gaagagaact gcctttggca 1320
280 gagttctata atgtaaaca tatcagactt ttttttttta taatcaagcc taaaattgta 1380
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284 aaagaaaatc tctgtgaaac ccctatgtgg aggcggaatt gctctcccag cccttgcatt 1500
286 gcagaggggc ccatgaaaga ggacaggcta cccctttaca aatagaattt gagcatcagt 1560
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290 cactgatgac tttttatact ttgtaaagac aattgttggg gagcccctca cacagccctg 1680
292 gcctctgctc aactagcaga tacagggatg aggcagacct gactctctta aggaggctga 1740
294 gagcccaaac tgctgtccca aacatgcact tccttgctta aggtatggta caagcaatgc 1800
296 ctgcccattg gagagaaaaa acttaagtag ataaggaaat aagaaccact cataattctt 1860
298 caccttagga ataatctcct gttaatatgg tgtacattct tcttgattat tttctacaca 1920
300 tacatgtaaa atatgtcttt ctttttttaa taggggtgta ctatgctgtt atgagtggct 1980
302 ttaatgaata aacatttgta gcctcctctt taatgggtaa acagcaaaaa aaaaaaaaaa 2040
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309 <210> SEQ ID NO: 5

310 <211> LENGTH: 198

311 <212> TYPE: PRT

312 <213> ORGANISM: Pongo pygmaeus

314 <400> SEQUENCE: 5

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320 His Ala Ala Arg Pro Ser Gln Phe Arg Val Ser Pro Leu Asp Arg Thr
321 20 25 30
324 Trp Asn Leu Gly Glu Thr Val Glu Leu Lys Cys Gln Val Leu Leu Ser
325 35 40 45
328 Asn Pro Thr Ser Gly Cys Ser Trp Leu Phe Gln Pro Arg Gly Ala Ala
329 50 55 60
332 Ala Ser Pro Thr Phe Leu Leu Tyr Leu Ser Gln Asn Lys Pro Lys Ala
333 65 70 75 80
336 Ala Glu Gly Leu Asp Thr Gln Arg Phe Ser Gly Lys Arg Leu Gly Asp
337 85 90 95
340 Thr Phe Val Leu Thr Leu Ser Asp Phe Arg Arg Glu Asn Glu Gly Tyr
341 100 105 110
344 Tyr Phe Cys Ser Ala Leu Ser Asn Ser Ile Met Tyr Phe Ser His Phe
345 115 120 125
348 Val Pro Val Phe Leu Pro Val His Thr Arg Gly Leu Asp Phe Ala Cys
349 130 135 140
352 Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
353 145 150 155 160
356 Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Arg Arg
357 165 170 175
360 Val Cys Lys Cys Pro Arg Pro Val Val Lys Ser Gly Gly Lys Pro Ser
361 180 185 190

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376 ccgagccagt tccgggtgtc gccctgggat cggacctgga acctgggcga gacggtggag      120
378 ctgaagtgcc aggtgctgct gtccaacccg acgtctggct gctcctggct cttccagccg      180
380 cgtggcgccg ccgccagtc caccctctct ctatacctct cccaaaacaa gccaaggcg      240
382 gccgaggggc tggacaccca gcggttctcg ggcaagaggt tgggggacac cttcgtcctc      300
384 accctgagcg acttcgcgcg ggagaacgaa ggctactatt tctgctcggc cctgagcaac      360
386 tccatcatgt acttcagcca cttegtgccg gtcttctctc cagtgcacac gagggggctg      420
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410 Glu Leu Arg Ile Phe Pro Lys Lys Met Asp Ala Glu Leu Gly Gln Lys
411      35      40      45
414 Val Asp Leu Val Cys Glu Val Leu Gly Ser Val Ser Gln Gly Cys Ser
415      50      55      60
418 Trp Leu Phe Gln Asn Ser Ser Lys Leu Pro Gln Pro Thr Phe Val
419 65      70      75      80
422 Val Tyr Met Ala Ser Ser His Asn Lys Ile Thr Trp Asp Glu Lys Leu
423      85      90      95
426 Asn Ser Ser Lys Leu Phe Ser Ala Met Arg Asp Thr Asn Asn Lys Tyr
427      100     105     110
430 Val Leu Thr Leu Asn Lys Phe Ser Lys Glu Asn Glu Gly Tyr Tyr Phe
431      115     120     125
434 Cys Ser Val Ile Ser Asn Ser Val Met Tyr Phe Ser Ser Val Val Pro
435      130     135     140
438 Val Leu Gln Lys Val Asn Ser Thr Thr Thr Lys Pro Val Leu Arg Thr
439 145     150     155     160
442 Pro Ser Pro Val His Pro Thr Gly Thr Ser Gln Pro Gln Arg Pro Glu
443      165     170     175
446 Asp Cys Arg Pro Arg Gly Ser Val Lys Gly Thr Gly Leu Asp Phe Ala
447      180     185     190
450 Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Ile Cys Val Ala Leu
451      195     200     205
454 Leu Leu Ser Leu Ile Ile Thr Leu Ile Cys Tyr His Arg Ser Arg Lys

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VERIFICATION SUMMARY

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